

LISTE DE SÉQUENCES.

NOMBRE DE SÉQUENCES : 6

5 INFORMATION CONCERNANT LA SEQ ID NO:1 :

i) CARACTERISTIQUE DE LA SEQUENCE :

A) LONGUEUR : 3562 paires de base

B) TYPE : acide nucléique

10 C) NOMBRE DE BRINS : double

D) CONFIGURATION : linéaire

ii) TYPE DE MOLECULE : ADN

vi) ORIGINE : rat

15

ix) CARACTERISTIQUE

A) NOM/CLE : ASIC

B) LOCALISATION : 123 .. 1700

20 xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:1 :

CACACACACA CACACACACA CACACACACA CACACACACA CACACAGAAC CTGCGCCTGT 60

GCCTGTGCCT GTGCGCTGTC CTGTTTGAGA GCTGGAGACA CAGAAGGATC CCCTTGCGAA 120

25 GG ATG GAA TTG AAG ACC GAG GAG GAG GAG GTG GGT GGT GTC CAG CCG 167
 Met Glu Leu Lys Thr Glu Glu Glu Glu Val Gly Gly Val Gln Pro 15
 1 5 10 15

30 GTG AGC ATC CAG GCT TTC GCC AGC AGC TCC ACG CTG CAT GGT CTT GCC 215
 Val Ser Ile Gln Ala Phe Ala Ser Ser Thr Leu His Gly Leu Ala 30
 20 25 30

35 CAC ATC TTC TCC TAT GAG CGG CTG TCT CTG AAG CGG GCA CTG TGG GCC 263
 His Ile Phe Ser Tyr Glu Arg Leu Ser Leu Lys Arg Ala Leu Trp Ala 45
 35 40 45

40 CTG TGC TTC CTG GGT TCG CTG GCC GTC CTG CTG TGT GTG TGC ACT GAG 311
 Leu Cys Phe Leu Gly Ser Leu Ala Val Leu Leu Cys Val Cys Thr Glu 60
 50 55 60

45 CGT GTG CAG TAC TAC TTC TGC TAT CAC CAC GTC ACC AAG CTT GAC GAA 359
 Arg Val Gln Tyr Tyr Phe Cys Tyr His His Val Thr Lys Leu Asp Glu 70 75
 65 70 75

GTG GCT GCC TCC CAG CTC ACC TTC CCT GCT GTC ACA CTG TGC AAT CTC 407
 Val Ala Ala Ser Gln Thr Phe Pro Ala Val Thr Leu Cys Asn Leu 95
 80 85 90 95

50 AAT GAG TTC CGC TTT AGC CAA GTC TCC AAG AAT GAC CTG TAC CAT GCT 455
 Asn Glu Phe Arg Phe Ser Gln Val Ser Lys Asn Asp Leu Tyr His Ala 110
 100 105 110

55 GGG GAG CTG CTG GCC CTG CTC AAC AAC AGG TAT GAG ATC CCG GAC ACA 503
 Gly Glu Leu Leu Ala Leu Leu Asn Asn Arg Tyr Glu Ile Pro Asp Thr 125
 115 120 125

	CAG ATG GCT GAT GAA AAG CAG CTA GAG ATA TTG CAG GAC AAG GCC AAC	551
	Gln Met Ala Asp Gln Lys Gln Leu Glu Ile Leu Gln Asp Lys Ala Asn	
	130 135 140	
5	TTC CGG AGC TTC AAG CCC AAG CCC TTC AAC ATG CGT GAA TTC TAC GAC	599
	Phe Arg Ser Phe Lys Pro Lys Pro Phe Asn Met Arg Glu Phe Tyr Asp	
	145 150 155	
10	AGA GCG GGG CAC GAT ATT CGA GAC ATG CTG CTC TCG TGC CAC TTC CGT	647
	Arg Ala Gly His Asp Ile Arg Asp Met Leu Ser Cys His Phe Arg	
	160 165 170 175	
	GGG GAG GCC TGC AGC GCT GAA GAT TTC AAA GTG GTC TTC ACT CGG TAT	695
	Gly Glu Ala Cys Ser Ala Glu Asp Phe Lys Val Val Phe Thr Arg Tyr	
15	180 185	
	GGG AAG TGT TAC ACA TTC AAC TCG GGC CAA GAT GGG CGG CCA CGG CTG	743
	Gly Lys Cys Tyr Thr Phe Asn Ser Gly Gln Asp Gly Arg Pro Arg Leu	
	195 200 205	
20	AAG ACC ATG AAA GGT GGG ACT GGC AAT GGC CTG GAG ATC ATG CTG GAC	791
	Lys Thr Met Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu Asp	
	210 215 220	
25	ATT CAG CAA GAT GAA TAT TTG GTG TGG GGA GAG ACC GAC GAG ACA	839
	Ile Gln Gln Asp Glu Tyr Leu Pro Val Trp Gly Glu Thr Asp Glu Thr	
	225 230 235	
30	TCC TTC GAA GCA GGC ATC AAA GTG CAG ATC CAC AGT CAG GAT GAA CCC	887
	Ser Phe Glu Ala Gly Ile Lys Val Gln Ile His Ser Gln Asp Glu Pro	
	240 245 250 255	
	CCT TTC ATC GAC CAG CTG GGC TTT GGT GTG GCT CCA GGT TTC CAG ACG	935
	Pro Phe Ile Asp Gln Leu Gly Phe Gly Val Ala Pro Gly Phe Gln Thr	
35	260 265 270	
	TTT GTG TCT TGC CAG GAG CAG AGG CTC ATC TAC CTG CCC TCA CCC TGG	983
	Phe Val Ser Cys Gln Glu Gln Arg Leu Ile Tyr Leu Pro Ser Pro Trp	
	275 280 285	
40	GGC ACC TGC AAT GCT GTT ACC ATG GAC TCG GAT TTC TTC GAC TCC TAC	1031
	Gly Thr Cys Asn Ala Val Thr Met Asp Ser Asp Phe Phe Asp Ser Tyr	
	290 295 300	
45	AGC ATC ACT GCC TGC CGG ATT GAT TGC GAG ACG CGT TAC CTG GTG GAG	1079
	Ser Ile Thr Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr Leu Val Glu	
	305 310 315	
50	AAC TGC AAC TGC CGT ATG GTG CAC ATG CCA GGG GAC GCC CCA TAC TGC	1127
	Asn Cys Asn Cys Arg Met Val His Met Pro Gly Asp Ala Pro Tyr Cys	
	320 325 330 335	
	ACT CCA GAG CAG TAC AAG GAG TGT GCA GAT CCT GCC CTG GAC TTC CTA	1175
	Thr Pro Glu Gln Tyr Lys Glu Cys Ala Asp Pro Ala Leu Asp Phe Leu	
55	340 345 350	
	GTG GAG AAA GAC CAG GAA TAC TGC GTG TGT GAG ATG CCT TGC AAC CTG	1223
	Val Glu Lys Asp Gln Glu Tyr Cys Val Cys Glu Met Pro Cys Asn Leu	
	355 360 365	

	ACC CGC TAC GGC AAG GAG CTG TCC ATG GTC AAG ATC CCA AGC AAA GCC Thr Arg Tyr Gly Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys Ala 370 375 380	1271
5	TCC GCC AAG TAC CTG GCC AAG AAG TTC AAC AAA TCG GAG CAG TAC ATA Ser Ala Lys Tyr Leu Ala Lys Lys Phe Asn Lys Ser Glu Gln Tyr Ile 385 390 395	1319
10	GGG GAG AAC ATT CTG GTG CTG GAC ATT TTC TTT GAA GTC CTC AAC TAT Gly Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Val Leu Asn Tyr 400 405 410 415	1367
15	GAG ACC ATC GAG CAG AAA AAG GCC TAT GAG ATC GCA GGG CTG TTG GGT Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly Leu Leu Gly 420 425 430	1415
20	GAC ATC GGG GGC CAG ATG GGG TTG TTC ATC GGT GCC AGC ATC CTC ACC Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu Thr 435 440 445	1463
25	GTG CTG GAA CTC TTT GAC TAT GCC TAC GAG GTC ATT AAG CAC AGG CTG Val Leu Glu Leu Phe Asp Tyr Ala Tyr Glu Val Ile Lys His Arg Leu 450 455 460	1511
30	TGC AGA CGT GGA AAG TGC CAG AAG GAG GCT AAG AGG AGC AGC GCA GAC Cys Arg Arg Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser Ser Ala Asp 465 470 475	1559
35	AAG GGC GTG GCG CTC AGC CTG GAT GAC GTC AAA AGA CAC AAT CCC TGC Lys Gly Val Ala Leu Ser Leu Asp Asp Val Lys Arg His Asn Pro Cys 480 485 490 495	1607
40	GAG AGC CTC CGA GGA CAT CCT GCC GGG ATG ACG TAC GCT GCC AAC ATC Glu Ser Leu Arg Gly His Pro Ala Gly Met Thr Tyr Ala Ala Asn Ile 500 505 510	1655
45	CTA CCT CAC CAT CCC GCT CGA GGC ACG TTT GAG GAC TTT ACC TGC TAA Leu Pro His His Pro Ala Arg Gly Thr Phe Glu Asp Phe Thr Cys * 515 520 526	1703
50	GCCCTCGCAG GCCGCTGTAC CAAAGGCCCTA GGTGGGGAGG GCTGGGGGAG CAAGGGGCCC CCAAGTGGCC CCAGCTACCC TGTTGGACTTA ACTGCATTCC TGGTCAGTGG TTCCCTCTTG TCTGTGGTGA GAAAGGAGTC TTGACCATAG AGTCCTCTCC CAGCCTCTAT CCCATCTTTT TATTTTAATT TAATCATT TGCTCTGTAA TATTGCTTGA GGCTGGGGAT CGTGATTTCC CCCCAGTTCT TTTATTGTTG AGAATAGTTT TCTCTATTCT GGGTTTTCTG TTATTTCAAA TGAATCTGCA AATTGCTCTT CCCATCTCTA TGAAGAATTG CGTTGGAATT TTGATGGGGA TTGTATTGAA TCTGTAGATT GCCTTTGGTA AGATGGCCAT TTTTACTATG TTAATCTGCG CAATTCATGA GCAAGGGAGA TCTTTCTATC TCTGAAATCT ACTTCAGTTT CTTTCTTCAG AGACTTGAAG TTCTTTGTCAT AAAAATCTTT TTGGTTAGAG CCACACCAAG GTATTTTATA TTGTTTGTGA CTATTGTGAA TGGTGTCAAT TCCCTAATTT CCTTCTCAGC CTACTTTATCC	1763 1823 1943 2003 2063 2123 2183 2243 2303 2363

	TTTGAGTAGA GGAAGGCTTC TGATTGTGTTT GGGTTAATTT TATACCCAGC TGCTTTGCTA	2423
	AAGTTCTTTA TCAGGTTTAG GTGTTCTCTG GTGGAACCTT TGGGGTCACG TAAGAATACT	2483
5	ATTATATCAT CTGCAAAATAG TGATATTCA CTCTCTCCTT TCCAATTTCT ATCCCTCTGG	2543
	GGACTTTTGT TTGTCCTAAT GCTCTGGCTA GGACTTCAAA TTCTATATTG AATAGATAGG	2603
10	GAGAGAGTGG GCAGCCTTGT CTAGTTCTCTG GTTTTCGTGG GATCGCTTCA AATTTCTCTC	2663
	CATTTAGTTT GATATTGGCT ACTGGTTTGC TGTATATGGC TTTTACTGTA CTTAGGTATG	2723
	GGCCTTGAAT TCCTGATATT TCCAAGACTT TTAACATGAA GGGGTTTGA AATTTGCCAA	2783
15	ATGCTTTCTC AGCATCTAAT GAGATGATCA TGTGCCCTCC CCCACCTTG AGTTTGTTTA	2843
	TATAGTGGGT TACATGAAA GATCATTCT AATAGTCCAC AAGTCTGCCA AATCTTGCTG	2903
20	ATTGTGACTC ATTTCCATAG CAGGCTCTAT AACTTCTCTA ACAGATTGCA TTAAACTCTG	2963
	CTTGGGGAAG GCATTACCTC TTGGTTGAAG CAATGTTGTA GTTTCTATGC CTGCTGAGTA	3023
	AATAGCCTCA AGTCCAAGTA CTTGCCCAGA CTAATGATCA AACGTATCCA GGAGTTCAT	3083
25	ACCAGAGATG TACTCTTCTC TCCTTTGAAG TACATTGCTG GAAGAGTAAT TGTGTTTGCT	3143
	AGAGATACTC CTTGCAACTG CAAAAGAAAT CTCTTGGCTA AGCATATAAT CAAGCCTCAG	3203
30	GTTTTCTTTT TATTAAATAG CTGCTTGTAA GAAAGTGGAC ACTAAGCATA TACCTCAAAG	3263
	GGAGACAGAA TGACTCTGTG CCTCCTACTGA TGGAAAGTCTG GGTACAAAT TACATCAGAA	3323
	GAACCTATCA TAGTGAAACA TCTCATTTCC CTGGTATAAT CCTTCTAGA AATACACTTG	3383
35	TGACTCTGAA ATGTTATAAT CGTGACAACT AGCTGTGTAC AGATACACCA AGTTAAATTT	3443
	GATAGAGAAA CCAGGCTTGG AGCCTCATGT CCATAGGGCA AGAGGAAGAT GCTGAGTGT	3503
	TAAGGTGTGT TTGAGCGAAG AACAAATACCT TGTGTCACAA AAATGAAAGG AAAAAAGAAA	3563
40	AAAGGAAAGA AGGAAAGAAA GAGAGAGAAA GAAAAAGAAA GAAAGAAAAA AAAAAAAA	3562

INFORMATION CONCERNANT LA SEQ ID NO:2 :

i) CARACTERISTIQUE DE LA SEQUENCE :

A) LONGUEUR : 1620 paires de base

B) TYPE : acide nucléique

C) NOMBRE DE BRINS : double

D) CONFIGURATION : linéaire

ii) TYPE DE MOLECULE : ADN

vi) ORIGINE : homme

ix) CARACTERISTIQUE

A) NOM/CLE : ASIC

B) LOCALISATION : 1 .. 1542

xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:2 :

CCG GTG AGC ATC CAG GCC TTC GCC AGC AGC TCC ACA CTG CAC GGC ATG	48
Pro Val Ser Ile Gln Ala Phe Ala Ser Ser Ser Thr Leu His Gly Met	
1 5 10 15	

GCC CAC ATC TTC TCC TAC GAG CGG CTG TCT CTG AAG CGG GCA CTG TGG	96
Ala His Ile Phe Ser Tyr Glu Arg Leu Ser Leu Lys Arg Ala Leu Trp	
20 25 30	

GCC CTG TGC TTC CTG GGC TCG CTG GCT GTG CTG CTG TGT GTG TGC ACG	144
Ala Leu Cys Phe Leu Gly Ser Leu Ala Val Leu Leu Cys Val Cys Thr	
35 40 45	

GAG CGT GTG CAG TAC TAC TTC CAC TAC CAC CAT GTC ACC AAG CTC GAC	192
Glu Arg Val Gln Tyr Tyr Phe His Tyr His His Val Thr Lys Leu Asp	
50 55 60	

GAG GTG GCT GCC TCT CAG CTT ACC TTC CCT GCT GTC ACG CTG TGC AAC	240
Glu Val Ala Ala Ser Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn	
65 70 75 80	

CTC AAC GAG TTC CGC TTT AGC CAA GTC TCC AAG AAT GAC CTG TAT CAT	288
Leu Asn Glu Phe Arg Phe Ser Gln Val Ser Lys Asn Asp Leu Tyr His	
85 90 95	

GCT GGG GAG CTG CTG GCC CTG CTC AAC AAC AGG TAT GAG ATA CCA GAC	336
Ala Gly Glu Leu Leu Ala Leu Leu Asn Asn Arg Tyr Glu Ile Pro Asp	
100 105 110	

ACA CAG ATG GCA GAT GAA AAG CAG CTG GAG ATA CTG CAG GAC AAA GCC	384
Thr Gln Met Ala Asp Glu Lys Gln Leu Glu Ile Leu Gln Asp Lys Ala	
115 120 125	

AAC TTC CGC AGC TTC AAA CCC AAA CCC TTC AAC ATG CGT GAG TTC TAC	432
Asn Phe Arg Ser Phe Lys Pro Lys Pro Phe Asn Met Arg Glu Phe Tyr	
130 135 140	

GAC CGA GCT GGG CAC GAC ATT CGA GAC ATG CTG CTC TCC TGC CAC TTC	480
Asp Arg Ala Gly His Asp Ile Arg Asp Met Leu Ser Cys His Phe	
145 150 155 160	

	CGG GGG GAG GTC TGC AGC GCT GAA GAC TTC AAG GTG GTC TTC ACA CGC Arg Gly Glu Val Cys Ser Ala Glu Asp Phe Lys Val Val Phe Thr Arg	528
	165	
5	TAT GGA AAG TGC TAC ACG TTC AAC TCG GGC CGA AAT GGG CGG CCG CGG Tyr Gly Lys Cys Tyr Thr Phe Asn Ser Gly Arg Asn Gly Arg Pro Arg	576
	180	
10	CTG AAG ACC ATG AAG GGT GGG ACG GGC AAT GGG CTG GAA ATC ATG CTG Leu Lys Thr Met Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu	624
	195	
	200	
15	GAC ATC CAG CAG GAC GAG TAC CTG CCT GTG TGG GGG GAG ACT GAC GAG Asp Ile Gln Gln Asp Glu Tyr Leu Pro Val Trp Gly Glu Thr Asp Glu	672
	210	
	215	
20	ACG TCT TTC GAA GCA GGC ATC AAA GTG CAG ATC CAT AGT CAG GAT GAA Thr Ser Phe Glu Ala Ile Lys Val Gln Ile His Ser Gln Asp Glu	720
	225	
	230	
	235	
25	CCT CCT TTC ATC GAC CAG CTG GGC TTT GGC GTG GCC CCA GGC TTC CAG Pro Pro Phe Ile Asp Gln Leu Gly Phe Gly Val Ala Pro Gly Phe Gln	768
	245	
	250	
30	ACC TTT GTG GCC TGC CAG GAG CAG CGG CTC ATA TAC CTG CCC CCA CCC Thr Phe Val Ala Cys Gln Glu Gln Arg Leu Ile Tyr Leu Pro Pro Pro	816
	260	
	265	
	270	
35	TGG GGC ACC TGC AAA GCT GTT ACC ATG GAC TCG GAT TTG GAT TTC TTC Trp Gly Thr Cys Lys Ala Val Thr Met Asp Ser Asp Leu Asp Phe Phe	864
	275	
	280	
	285	
40	GAC TCC TAC AGC ATC ACT GCC TGC CGC ATC GAC TGT GAG ACG CGC TAC Asp Ser Tyr Ser Ile Thr Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr	912
	290	
	295	
	300	
45	CTG GTG GAG AAC TGC AAC TGC CGC ATG GTG CAC ATG CCA GGG GAT GCC Leu Val Glu Asn Cys Asn Cys Arg Met Val His Met Pro Gly Asp Ala	960
	305	
	310	
	315	
50	CCA TAC TGT ACT CCA GAG CAG TAC AAG GAG TGT GCA GAT CCT GCT CTG Pro Tyr Cys Thr Pro Glu Gln Tyr Lys Glu Cys Ala Asp Pro Ala Leu	1008
	325	
	330	
	335	
55	GAC TTC CTG GTG GAG AAG GAC CAG GAG TAC TGC GTG TGT GAA ATG CCT Asp Phe Leu Val Glu Lys Asp Gln Glu Tyr Cys Val Cys Glu Met Pro	1056
	340	
	345	
	350	
60	TGC AAC CTG ACC CGC TAT GGC AAA GAG CTG TCC ATG GTC AAG ATC CCC Cys Asn Leu Thr Arg Tyr Gly Lys Glu Leu Ser Met Val Lys Ile Pro	1104
	355	
	360	
	365	
65	AGC AAA GCC TCA GCC AAG TAC CTG GCC AAG AAG TTC AAC AAA TCT GAG Ser Lys Ala Ser Ala Lys Tyr Leu Ala Lys Lys Phe Asn Lys Ser Glu	1152
	370	
	375	
	380	
70	CAA TAC ATA GGG GAG AAC ATC CTG GTG CTG GAC ATT TTC TTT GAA GTC Gln Tyr Ile Gly Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Val	1200
	385	
	390	
	395	
	400	

	CTC AAC TAT GAG ACC ATT GAA CAG AAG AAG GCC TAT GAG ATT GCA GGG Leu Asn Tyr Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly 405 410 415	1248
5	CTC CTG GGT GAC ATC GGG GGC CAG ATG GGG CTG TTC ATC GGG GCC AGC Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser 420 425 430	1296
10	ATC CTC ACG GTG CTG GAG CTC TTT GAC TAC GCC TAC GGG GTC ATT AAG Ile Leu Thr Val Leu Glu Leu Phe Asp Tyr Ala Tyr Gly Val Ile Lys 435 440 445	1344
15	CAC AAG CTG TGC CGA CGA GGA AAA TGC CAG AAG GAG GCC AAA AGG AGC His Lys Leu Cys Arg Arg Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser 450 455 460	1392
20	AGT GCG GAC AAG GGC GTG GCC CTC AGC CTG GAC GAC GTC AAA AGA CAC Ser Ala Asp Lys Gly Val Ala Leu Ser Leu Asp Asp Val Lys Arg His 465 470 475 480	1440
25	AAC CCG TGC GAG AGC CTT CGG GGC CAC CCT GCC GGG ATG ACA TAC GCT Asn Pro Cys Glu Ser Leu Arg Gly His Pro Ala Gly Met Thr Tyr Ala 485 490 495	1488
30	GCC AAC ATC GTA CCT CAC CAT CCG GCC CGA GGC ACG TTC GAG GAC TTT Ala Asn Ile Val Pro His His Pro Ala Arg Gly Thr Phe Glu Asp Phe 500 505 510	1536
35	ACC TGC TGA GCCCGCAGG CGCCCGAACC AAAGACCTAG ATGGGGAGGA CTAGGAGAGC Thr Cys * 514	1595
	GAGGGGGCCC CCAGCTGCCT CCTAA	1620

INFORMATION CONCERNANT LA SEQ ID NO:3 :

i) CARACTERISTIQUE DE LA SEQUENCE :
 5 A) LONGUEUR : 1666 paires de base
 B) TYPE : acide nucléique
 C) NOMBRE DE BRINS : double
 D) CONFIGURATION : linéaire

 ii) TYPE DE MOLECULE : ADN
 10 vi) ORIGINE : homme

 ix) CARACTERISTIQUE
 A) NOM/CLE : MDEG
 B) LOCALISATION : 127 .. 1663
 15 xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:3 :

	TCTGGCGCGA TGCTTACCTT GCGTTCTCTC CCCTGAACGT CAAGGTTTAA GCAGAGCCCG	60
20	AGGACTGGGA GCTCTTCTCT GAAATTCGAT CAACCTGAAG CCAGTTGCGG AACTGCACGG	120
	GGTCCCG ATG GAC CTC AAG GAA AGC CCC AGT GAG GGC AGC CTG CAA CCT Met Asp Leu Lys Glu Ser Pro Ser Glu Gly Ser Leu Gln Pro 1 5 10	169
25	TCT AGC ATC CAG ATC TTT GCC AAC ACC TCC ACC CTC CAT GGC ATC CGC Ser Ser Ile Gln Ile Phe Ala Asn Thr Ser Thr Leu His Gly Ile Arg 15 20 25 30	217
30	CAC ATC TTC GTG TAT GGG CCG CTG ACC ATC CGG CGT GTG CTG TGG GCA His Ile Phe Val Tyr Gly Pro Leu Thr Ile Arg Arg Val Leu Trp Ala 35 40 45	265
35	GTG GCC TTC GTG GGC TCT CTG GGC CTG CTG CTG GTG GAG AGC TCT GAG Val Ala Phe Val Gly Ser Leu Gly Leu Leu Leu Val Glu Ser Ser Glu 50 55 60	313
40	AGG GTG TCC TAC TAC TTC TCC TAC CAG CAT GTC ACT AAG GTG GAC GAA Arg Val Ser Tyr Tyr Phe Ser Tyr Gln His Val Thr Lys Val Asp Glu 65 70 75	361
45	GTG GTG GCT CAA AGC CTG GTC CCA GCT GTG ACC CTC TGT AAC CTC Val Val Ala Gln Ser Leu Val Phe Pro Ala Val Thr Leu Cys Asn Leu 80 85 90	409
	AAT GGC TTC CGG TTC TCC AGG CTC ACC ACC AAC GAC CTG TAC CAT GCT Asn Gly Phe Arg Phe Ser Arg Leu Thr Thr Asn Asp Leu Tyr His Ala 95 100 105 110	457
50	GGG GAG CTG CTG GCC CTG CTG GAT GTC AAC CTG CAG ATC CCG GAC CCC Gly Glu Leu Leu Ala Leu Leu Asp Val Asn Leu Gln Ile Pro Asp Pro 115 120 125	505
55	CAT CTG GCT GAC CCC TCC GTG CTG GAG GCC CTG CGG CAG AAG GCC AAC His Leu Ala Asp Pro Ser Val Leu Glu Ala Leu Arg Gln Lys Ala Asn 130 135 140	553

	TTC	AAG	CAC	TAC	AAA	CCC	AAG	CAG	TTC	AGC	ATG	CTG	GAG	TTC	CTG	CAC	601
	Phe	Lys	His	Tyr	Lys	Pro	Lys	Gln	Phe	Ser	Met	Leu	Glu	Phe	Leu	His	
			145					150					155				
5	CGT	GTG	GGC	CAT	GAC	CTG	AAG	GAT	ATG	ATG	CTC	TAC	TGC	AAG	TTC	AAA	649
	Arg	Val	Gly	His	Asp	Leu	Lys	Asp	Met	Met	Leu	Tyr	Cys	Lys	Phe	Lys	
		160					165					170					
10	GGG	CAG	GAG	TGC	GGC	CAC	CAA	GAC	TTC	ACC	ACA	GTG	TTT	ACA	AAA	TAT	697
	Gly	Gln	Glu	Cys	Gly	His	Gln	Asp	Phe	Thr	Thr	Val	Phe	Thr	Lys	Thr	
		175				180					185				190		
15	GGG	AAG	TGT	TAC	ATG	TTT	AAC	TCA	GGC	GAG	GAT	GGC	AAA	CCT	CTG	CTC	745
	Gly	Lys	Cys	Tyr	Met	Phe	Asn	Ser	Gly	Glu	Asp	Gly	Lys	Pro	Leu	Leu	
					195					200					205		
20	ACC	ACG	GTC	AAG	GGG	GGG	ACA	GGC	AAC	GGG	CTG	GAG	ATC	ATG	CTG	GAC	793
	Thr	Thr	Val	Lys	Gly	Gly	Thr	Gly	Asn	Gly	Leu	Glu	Ile	Met	Leu	Asp	
				210					215					220			
25	ATT	CAG	CAG	GAT	GAG	TAC	CTG	CCC	ATC	TGG	GGA	GAG	ACA	GAG	GAA	ACG	841
	Ile	Gln	Gln	Asp	Glu	Tyr	Leu	Pro	Ile	Trp	Gly	Glu	Thr	Glu	Glu	Thr	
				225				230					235				
30	ACA	TTT	GAA	GCA	GGA	GTG	AAA	GTT	CAG	ATC	CAC	AGT	CAG	TCT	GAG	CCA	889
	Thr	Phe	Glu	Ala	Gly	Val	Lys	Val	Gln	Ile	His	Ser	Gln	Ser	Glu	Pro	
			240				245					250					
35	CCT	TTC	ATC	CAA	GAG	CTG	GGC	TTT	GGG	GTG	GCT	CCA	GGG	TTC	CAG	ACC	937
	Pro	Phe	Ile	Gln	Glu	Leu	Gly	Phe	Gly	Val	Ala	Pro	Gly	Phe	Gln	Thr	
			255			260					265				270		
40	TTT	GTG	GCC	ACA	CAG	GAG	CAG	AGG	CTC	ACA	TAC	CTG	CCC	CCA	CCG	TGG	985
	Phe	Val	Ala	Thr	Gln	Glu	Gln	Arg	Leu	Thr	Tyr	Leu	Pro	Pro	Pro	Trp	
				275					280						285		
45	GGT	GAG	TGC	CGA	TCC	TCA	GAG	ATG	GGC	CTC	GAC	TTT	TTT	CCT	GTT	TAC	1033
	Gly	Glu	Cys	Arg	Ser	Ser	Glu	Met	Gly	Leu	Asp	Phe	Phe	Pro	Val	Tyr	
				290					295					300			
50	AGC	ATC	ACC	GCC	TGT	AGG	ATT	GAC	TGT	GAG	ACC	CGC	TAC	ATT	GTG	GAA	1081
	Ser	Ile	Thr	Ala	Cys	Arg	Ile	Asp	Cys	Glu	Thr	Arg	Tyr	Ile	Val	Glu	
				305				310						315			
55	AAC	TGC	AAC	TGC	CGC	ATG	GTT	CAC	ATG	CCA	GGG	GAT	GCC	CCT	TTT	TGT	1129
	Asn	Cys	Asn	Cys	Arg	Met	His	Met	Pro	Gly	Asp	Ala	Pro	Phe	Cys		
				320			325					330					
60	ACC	CCT	GAG	CAG	CAC	AAG	GAG	TGT	GCA	GAG	CCT	GCC	CTA	GGT	CTG	TTG	1177
	Thr	Pro	Glu	Gln	His	Lys	Glu	Cys	Ala	Glu	Pro	Ala	Leu	Gly	Leu	Leu	
						340					345				350		
65	GCG	GAA	AAG	GAC	AGC	AAT	TAC	TGT	CTC	TGC	AGG	ACA	CCC	TGC	AAC	CTA	1225
	Ala	Glu	Lys	Asp	Ser	Asn	Tyr	Cys	Leu	Cys	Arg	Thr	Pro	Cys	Asn	Leu	
					355					360					365		
70	ACC	CGC	TAC	AAC	AAA	GAG	CTC	TCC	ATG	GTG	AAG	ATC	CCC	AGC	AAG	ACA	1273
	Thr	Arg	Tyr	Asn	Lys	Glu	Leu	Ser	Met	Val	Lys	Ile	Pro	Ser	Lys	Thr	
				370					375					380			

2

3

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INFORMATION CONCERNANT LA SEQ ID NO:4 :

i) CARACTERISTIQUE DE LA SEQUENCE :
 A) LONGUEUR : 3647 paires de base
 5 B) TYPE : acide nucléique
 C) NOMBRE DE BRINS : double
 D) CONFIGURATION : linéaire

ii) TYPE DE MOLECULE : ADN
 10 vi) ORIGINE : rat

ix) CARACTERISTIQUE
 A) NOM/CLE : ASIC1B
 B) LOCALISATION : 109 .. 1785

15 xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:4 :

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CTGCCACAGA GGCTCTGGTG AGGAAGGACA GACAGCTGGA CCGGCGCAGA CCTAGCCGAA      60
20 GTCCAACCTC CGTCCCTTCT GGTGGCTTCT TCCTGTCTCC TGAACAAG  ATG CCC ATC      117
    Met Pro Ile
    1          3

CAG ATC TTT TGT TCT GTG TCA TTC TCC TCT GGA GAG GAG GCC CCG GGA      165
25 Gln Ile Phe Cys Ser Val Ser Phe Ser Ser Gly Glu Glu Ala Pro Gly
    5          10          15

TCC ATG GCA GAT ATC TGG GGT CCC CAC CAC CAC CGG CAG CAG CAG GAC      213
30 Ser Met Ala Asp Ile Trp Gly Pro His His His Arg Gln Gln Gln Asp
    20          25          30          35

AGC TCA GAA TCG GAA GAA GAG GAA GAG AAG GAA ATG GAG GCA GGG TCG      261
    Ser Ser Glu Ser Glu Glu Glu Glu Glu Lys Glu Met Glu Ala Gly Ser
    40          45          50

GAG TTG GAT GAG GGT GAT GAC TCA CCT AGG GAC TTG GTG GCC TTC GCC      309
    Glu Leu Asp Glu Gly Asp Asp Ser Pro Arg Asp Leu Val Ala Phe Ala
    55          60          65

AAC AGC TGT ACC TTC CAT GGT GCC AGC CAT GTG TTT GTG GAA GGG GGC      357
40 Asn Ser Cys Thr Phe His Gly Ala Ser His Val Phe Val Glu Gly Gly
    70          75          80

CCA GGG CCA AGG CAG GCC TTA TGG GCA GTG GCC TTT GTC ATA GCA CTG      405
45 Pro Gly Pro Arg Gln Ala Leu Trp Ala Val Ala Phe Val Ile Ala Leu
    85          90          95

GGT GCC TTC CTG TGC CAG GTA GGG GAC CGC GTT GCT TAT TAC CTC AGC      453
50 Gly Ala Phe Leu Cys Gln Val Gly Asp Arg Val Ala Tyr Tyr Leu Ser
    100          105          110          115

TAC CCA CAC GTG ACT TTG CTA GAC GAA GTG GCC ACC ACG GAG CTG GTC      501
    Tyr Pro His Val Thr Leu Leu Asp Glu Val Ala Thr Thr Glu Leu Val
    120          125          130
  
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	TTC CCA GCT GTC ACC TTC TGC AAC ACC AAT GCC GTG CGG TTG TCC CAG	549
	Phe Pro Ala Val Thr Phe Cys Asn Thr Asn Ala Val Arg Leu Ser Gln	
	135 140 145	
5	CTC AGC TAC CCT GAC TTG CTC TAC CTG GCC CCC ATG CTA GGA CTG GAT	597
	Leu Ser Tyr Pro Asp Leu Leu Tyr Leu Ala Pro Met Leu Gly Leu Asp	
	150 155 160	
10	GAG AGT GAT GAC CCC GGG GTG CCC CTT GCT CCT CCT GGC CCA GAG GCT	645
	Glu Ser Asp Asp Pro Gly Val Pro Leu Ala Pro Pro Gly Pro Glu Ala	
	165 170 175	
15	TTC TCC GGG GAG CCT TTT AAC CTC CAT CGT TTC TAT AAT CGC TCT TGC	693
	Phe Ser Gly Glu Pro Phe Asn Leu His Arg Phe Tyr Asn Arg Ser Cys	
	180 185 190 195	
	CAC CGG CTG GAG GAC ATG CTG CTC TAT TGT TCC TAC TGT GGG GGC CCC	741
	His Arg Leu Glu Asp Met Leu Leu Tyr Cys Ser Tyr Cys Gly Gly Pro	
	200 205 210	
20	TGT GGT CCC CAC AAC TTC TCA GTG GTC TTC ACT CGG TAT GGG AAG TGT	789
	Cys Gly Pro His Asn Phe Ser Val Val Phe Thr Arg Tyr Gly Lys Cys	
	215 220 225	
25	TAC ACA TTC AAC TCG GGC CAA GAT GGG CGG CCA CGG CTG AAG ACC ATG	837
	Tyr Thr Phe Asn Ser Gly Gln Asp Gly Arg Pro Arg Leu Lys Thr Met	
	230 235 240	
30	AAA GGT GGG ACT GGC AAT GGC CTG GAG ATC ATG CTG GAC ATT CAG CAA	885
	Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu Asp Ile Gln Gln	
	245 250 255	
35	GAT GAA TAT TTG CCT GTG TGG GGA GAG ACC GAC GAG ACA TCC TTC GAA	933
	Asp Glu Tyr Leu Pro Val Trp Gly Glu Thr Asp Glu Thr Ser Phe Glu	
	260 265 270 275	
40	GCA GGC ATC AAA GTG CAG ATC CAC AGT CAG GAT GAA CCC CCT TTC ATC	981
	Ala Gly Ile Lys Val Gln Ile His Ser Gln Asp Glu Pro Pro Phe Ile	
	280 285 290	
45	GAC CAG CTG GGC TTT GGT GTG GCT CCA GGT TTC CAG ACG TTT GTG TCT	1029
	Asp Gln Leu Gly Phe Gly Val Ala Pro Gly Phe Gln Thr Phe Val Ser	
	295 300 305	
50	TGC CAG GAG CAG AGG CTC ATC TAC CTG CCC TCA CCC TGG GGC ACC TGC	1077
	Cys Gln Glu Gln Arg Leu Ile Tyr Leu Pro Ser Pro Trp Gly Thr Cys	
	310 315 320	
55	AAT GCT GTT ACC ATG GAC TCG GAT TTC TTC GAC TCC TAC AGC ATC ACT	1125
	Asn Ala Val Thr Met Asp Ser Asp Phe Phe Asp Ser Tyr Ser Ile Thr	
	325 330 335	
55	GCC TGC CGG ATT GAT TGC GAG ACG CGT TAC CTG GTG GAG AAC TGC AAC	1173
	Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr Leu Val Glu Asn Cys Asn	
	340 345 350 355	

	TGC CGT ATG GTG CAC ATG CCA GGG GAC GCC CCA TAC TGC ACT CCA GAG	1221
	Cys Arg Met Val His Met Pro Gly Asp Ala Pro Tyr Cys Thr Pro Glu	
	360 365 370	
5	CAG TAC AAG GAG TGT GCA GAT CCT GCC CTG GAC TTC CTA GTG GAG AAA	1269
	Gln Tyr Lys Glu Cys Ala Asp Pro Ala Leu Asp Phe Leu Val Glu Lys	
	375 380 385	
10	GAC CAG GAA TAC TGC GTG TGT GAG ATG CCT TGC AAC CTG ACC CGC TAC	1317
	Asp Gln Glu Tyr Cys Val Cys Glu Met Pro Cys Asn Leu Thr Arg Tyr	
	390 395 400	
15	GGC AAG GAG CTG TCC ATG GTC AAG ATC CCA AGC AAA GCC TCC GCC AAG	1365
	Gly Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys Ala Ser Ala Lys	
	405 410 415	
	TAC CTG GCC AAG AAG TTC AAC AAA TCG GAG CAG TAC ATA GGG GAG AAC	1413
	Tyr Leu Ala Lys Lys Phe Asn Lys Ser Glu Gln Tyr Ile Gly Glu Asn	
	420 425 430 435	
20	ATT CTG GTG CTG GAC ATT TTC TTT GAA GTC CTC AAC TAT GAG ACC ATC	1461
	Ile Leu Val Leu Asp Ile Phe Phe Glu Val Leu Asn Tyr Glu Thr Ile	
	440 445 450	
25	GAG CAG AAA AAG GCC TAT GAG ATC GCA GGG CTG TTG GGT GAC ATC GGG	1509
	Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly Leu Leu Gly Asp Ile Gly	
	455 460 465	
30	GGC CAG ATG GGG TTG TTC ATC GGT GCC AGC ATC CTC ACC GTG CTG GAA	1557
	Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu Thr Val Leu Glu	
	470 475 480	
35	CTC TTT GAC TAT GCC TAC GAG GTC ATT AAG CAC AGG CTG TGC AGA CGT	1605
	Leu Phe Asp Tyr Ala Tyr Glu Val Ile Lys His Arg Leu Cys Arg Arg	
	485 490 495	
40	GGA AAG TGC CAG AAG GAG GCT AAG AGG AGC AGC GCA GAC AAG GGC GTG	1653
	Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser Ser Ala Asp Lys Gly Val	
	500 505 510 515	
	GCG CTC AGC CTG GAT GAC GTC AAA AGA CAC AAT CCC TGC GAG AGC CTC	1701
	Ala Leu Ser Leu Asp Asp Val Lys Arg His Asn Pro Cys Glu Ser Leu	
	520 525 530	
45	CGA GGA CAT CCT GCC GGG ATG ACG TAC GCT GCC AAC ATC CTA CCT CAC	1749
	Arg Gly His Pro Ala Gly Met Thr Tyr Ala Ala Asn Ile Leu Pro His	
	535 540 545	
50	CAT CCC GCT CGA GGC ACG TTT GAG GAC TTT ACC TGC TAA GCCCTCGCAG	1798
	His Pro Ala Arg Gly Thr Phe Glu Asp Phe Thr Cys *	
	550 55 559	
	GCCGCTGTAC CAAAGGCCTA GGTGGGGAGG GCTGGGGGAG CAAGGGGCCC CCAACTGCCC	1858
55	CCAGCTACCC TGTTGAGCTTA ACTGCATTCC TGTCAGTGG TTCCCTCTTG TCTGTGGTGA	1918
	GAAAGGAGTC TTGACCATAG AGTCCTCTCC CAGCCTCTAT CCCATCTTTT TATTTTAATT	1978
	TAATCACATT TGCTCTGTAA TATGTCTTGA GGCTGGGGAT CGTGATTTC CCCCAGTTCT	2038

	TTTATTGTTG AGAATAGTTT TCTCTATTCT GGGTTTTCTG TTATTTCAAA TGAATCTGCA	2098
	AATTGCTCTT CCCATCTCTA TGAAGAATTG CGTTGGAATT TTGATGGGGA TTGATTTGAA	2158
5	TCTGTAGATT GCCTTTGGTA AGATGGCCAT TTTTACTATG TTAATCTCGC CAATTCTATGA	2218
	GCAAGGAGA TCCTTCTATC TCTGAAATCT ACTTCAGTTT CTTTCTCTAG AGACTTGAAG	2278
10	TTCTTGTGAT AAAATCTTT TTGGTTAGAG CCACACCAAG GTATTTTATA TTGTTTGTA	2338
	CTATTGTGAA TGGTGTGATT TCCCTAATTT CCTTCTCAGC CTACTTATCC TTTGAGTAGA	2398
	GGAAGGCTTC TGATTGTTT GGGTTAATTT TATACCCAGC TGCTTTGCTA AAGTCTTTTA	2458
15	TCAGGTTTAG GTGTTCTCTG GTGGAACTTT TGGGGTCACG TAAGAATACT ATTATATCAT	2518
	CTGCAAAATG TGATATTTCA CTCTCTCCTT TCCAATTCT ATCCCTCTGG GGACTTTTTG	2578
20	TTGTCTAATT GCTCTGGCTA GGACTTCAAA TTCTATATTG AATAGATAGG GAGAGAGTGG	2638
	GCAGCCTTGT CTAGTTCCTG GTTTTCGTGG GATCGCTTCA AATTCTCTC CATTAGTTT	2698
	GATATTGGCT ACTGGTTTGC TGTATATGGC TTTTACTGTA CTTAGGTATG GGCCTTGAAT	2758
25	TCCTGATATT TCCAAGACTT TTAACATGAA GGGGTTTGA AATTGGCAA ATGCTTCTC	2818
	AGCATCTAAT GAGATGATCA TGTGCCCTCC CCCACCTTG AGTTTGTTTA TATAGTGGGT	2878
30	TACATGAAAG GATCATTCTT AATAGTCCAC AAGTCTGCCA AATCTTGCTG ATTGTGACTC	2938
	ATTTCATAG CAGGCTCTAT AACTTCTCTA ACAGATTGCA TTAAACTCTG CTTGGGGAAG	2998
	GCATTACCTC TTGGTTGAAG CAATGTTGTA GTTCTATGC CTGCTGAGTA AATAGCCTCA	3058
35	AGTCCAAGTA CTTGCCCAGA CTAATGATCA AACGTATCCA GGAGTTCAT ACCAGAGATG	3118
	TACTCTTCTC TCCTTTGAAG TACATTGCTG GAAGAGTAAT TGTGTTTGCT AGAGATACTC	3178
	CTTCGAACTG CAAAAGAAAT CTCTTGCTA AGCATATAAT CAAGCCTCAG GTTTTCTTTT	3238
40	TATTAAATAG TGCTTGTGTA GAAAGTGGAC ACTAAGCATA TACCTCAAAG GGAGACAGAA	3298
	TGACTCTGTG CCTTCACTGA TGGAGTCTG GGTACAAAT TACATCAGAA GAACCTATCA	3358
45	TAGTGAAACA TCTCATTTCC CTGGTATAAT CCCTTCTAGA AATACACTTG TGACTCTGAA	3418
	ATGTTATAAT CGTGACAACT AGGCTGTTAC AGATACACCA AGTTAAATTT GATAGAGAAA	3478
50	CCAGGCTTGG AGCCTCATGT CCATAGGCA AGAGGAAGAT GCTGAGTGT TAAGTTGGT	3538
	TTGAGCGAAG AACAATACCT TGTGTCACAA AATGAAAGG AAAAAAGAAA AAAGGAAAGA	3598
	AGGAAAGAAA GAGAGAGAAA GAAAAAGAAA GAAAGAAAAA AAAAAAAA	3647

INFORMATION CONCERNANT LA SEQ ID NO:5 :

i) CARACTERISTIQUE DE LA SEQUENCE :

A) LONGUEUR 1602 paires de base

B) TYPE : acide nucléique

C) NOMBRE DE BRINS : double

D) CONFIGURATION : linéaire

ii) TYPE DE MOLECULE : ADN

vi) ORIGINE : rat

ix) CARACTERISTIQUE

A) NOM/CLE : DRASIC

B) LOCALISATION : 1 .. 1602

xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:5 :

ATG AAA CCT CGC TCC GGA CTG GAG GAG GCC CAG CGG CGA CAG GCC TCA	48
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Met Lys Pro Arg Ser Gly Leu Glu Glu Ala Gln Arg Arg Gln Ala Ser	
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1 5 10 15	
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GAC ATC CGG GTG TTT GCC AGC AGC TGC ACA ATG CAT GGT CTG GGC CAC	96
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Asp Ile Arg Val Phe Ala Ser Ser Cys Thr Met His Gly Leu Gly His	
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20 25	
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ATC TTT GGC CCT GGA GGC CTG ACC CTG CGC CGA GGG CTG TGG GCC ACA	144
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Ile Phe Gly Pro Gly Gly Leu Thr Leu Arg Arg Gly Leu Trp Ala Thr	
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35 40 45	
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GCT GTG CTC CTG TCG CTG GCG GCC TTC CTC TAC CAG GTG GCT GAG CGG	192
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Ala Val Leu Leu Ser Leu Ala Ala Phe Leu Tyr Gln Val Ala Glu Arg	
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50 55 60	
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GTT CGC TAC TAT GGG GAG TTC CAC CAT AAG ACC ACC CTG GAT GAG CGT	240
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Val Arg Tyr Tyr Gly Glu Phe His His Lys Thr Thr Leu Asp Glu Arg	
---	--

65 70 75 80	
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GAG AGC CAC CAG CTC ACC TTC CCA GCT GTG ACT CTG TGT AAT ATC AAC	288
---	-----

Glu Ser His Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn Ile Asn	
---	--

40 85 90 95	
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CCA CTG CGC CGC TCA CGC CTC ACA CCC AAT GAC TTG CAC TGG GCT GGA	336
---	-----

Pro Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp Leu His Trp Ala Gly	
---	--

100 105 110	
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ACA GCG CTG CTG GGC CTG GAC CCT GCT GAA CAT GCT GCC TAC CTT CGT	384
---	-----

Thr Ala Leu Leu Gly Leu Asp Pro Ala Glu His Ala Ala Tyr Leu Arg	
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115 120 125	
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GCA CTG GGC CAG CCC CCC GCA CCA CCT GGC TTC ATG CCC AGT CCG ACC	432
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Ala Leu Gly Gln Pro Pro Ala Pro Pro Gly Phe Met Pro Ser Pro Thr	
---	--

130 135 140	
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TTT GAC ATG GCA CAA CTC TAC GCC AGA GCC GGC CAC TCC CTT GAG GAC	480
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Phe Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly His Ser Leu Glu Asp	
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145 150 155 160	
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	ATG TTG TTG GAT TGC CGA TAC CGT GGC CAG CCC TGT GGG CCT GAG AAC	528
	Met Leu Leu Asp Cys Arg Tyr Arg Gly Gln Pro Cys Gly Pro Glu Asn	
	165 170 175	
5	TTC ACA GTG ATC TTT ACT CGA ATG GGG CAA TGC TAC ACC TTC AAC TCT	576
	Phe Thr Val Ile Phe Thr Arg Met Gly Gln Cys Tyr Thr Phe Asn Ser	
	180 185 190	
10	GGT GCC CAC GGT GCA GAG CTG CTC ACC ACT CCA AAG GGT GGT GCT GGC	624
	Gly Ala His Gly Ala Glu Leu Thr Thr Pro Lys Gly Gly Ala Gly	
	195 200 205	
15	AAC GGA CTG GAG ATT ATG CTA GAT GTA CAG CAA GAG GAG TAT CTG CCC	672
	Asn Gly Leu Glu Ile Met Leu Asp Val Gln Gln Glu Tyr Leu Pro	
	210 215 220	
20	ATC TGG AAG GAC ATG GAA GAG ACC CCG TTT GAG GTG GGG ATC CGA GTG	720
	Ile Trp Lys Asp Met Glu Glu Thr Pro Phe Glu Val Gly Ile Arg Val	
	225 230 235 240	
25	CAG ATT CAC AGC CAG GAT GAG CCC CCT GCC ATT GAC CAG CTG GGC TTC	768
	Gln Ile His Ser Gln Asp Glu Pro Pro Ala Ile Asp Gln Leu Gly Phe	
	245 250 255	
30	GGG GCA GCC CCA GGC CAT CAG ACT TTT GTG TCC TGT CAG CAG CAG CAA	816
	Gly Ala Ala Pro Gly His Gln Thr Phe Val Ser Cys Gln Gln Gln	
	260 265 270	
35	CTG AGT TTC CTG CCA CCA CCC TGG GGT GAC TGC AAT ACC GCA TCT TTG	864
	Leu Ser Phe Leu Pro Pro Trp Gly Asp Cys Asn Thr Ala Ser Leu	
	275 280 285	
40	GAT CCC GAC GAC TTT GAT CCA GAG CCC TCT GAT CCC TTG GGT TCC CCC	912
	Asp Pro Asp Asp Phe Asp Pro Glu Pro Ser Asp Pro Leu Gly Ser Pro	
	290 295 300	
45	AGA CCC AGA CCC AGC CCT CCT TAT AGT TTA ATA GGT TGT CGC CTG GCC	960
	Arg Pro Arg Pro Ser Pro Pro Tyr Ser Leu Ile Gly Cys Arg Leu Ala	
	305 310 315 320	
50	TGT GAG TCT CGC TAT GTG GCT CGG AAG TGT GGC TGT CGA ATG ATG CAT	1008
	Cys Glu Ser Arg Tyr Val Ala Arg Lys Cys Gly Cys Arg Met Met His	
	325 330 335	
55	ATG CCT GGA AAC TCC CCA GTG TGC AGC CCC CAG CAG TAC AAG GAC TGC	1056
	Met Pro Gly Asn Ser Pro Val Cys Ser Pro Gln Gln Tyr Lys Asp Cys	
	340 345 350	
60	GCC AGC CCA GCT CTG GAC GCT ATG CTG CGA AAG GAC ACG TGT GTC TGC	1104
	Ala Ser Pro Ala Leu Asp Ala Met Leu Arg Lys Asp Thr Cys Val Cys	
	355 360 365	
65	CCC AAC CCG TGC GCT ACT ACA CGC TAT GCC AAG GAG CTC TCC ATG GTG	1152
	Pro Asn Pro Cys Ala Thr Arg Tyr Ala Lys Glu Leu Ser Met Val	
	370 375 380	
70	CGG ATT CCC AGC CGC GCG TCA GCT CGC TAC CTG GCC CGG AAA TAC AAC	1200
	Arg Ile Pro Ser Arg Ala Ser Ala Arg Tyr Leu Ala Arg Lys Tyr Asn	
	385 390 395 400	

	CGC AGC GAG TCC TAC ATT ACG GAG AAT GTA CTG GTT CTG GAT ATC TTC	1248
	Arg Ser Glu Ser Tyr Ile Thr Glu Asn Val Leu Val Leu Asp Ile Phe	
	405 410 415	
5	TTT GAG GCC CTC AAC TAT GAA GCG GTG GAA CAA AAG GCG GCC TAT GAA	1296
	Phe Glu Ala Leu Asn Tyr Glu Ala Val Glu Gln Lys Ala Ala Tyr Glu	
	420 425 430	
10	GTG TCG GAG CTG CTG GGA GAC ATT GGG GGA CAG ATG GGA CTG TTT ATT	1344
	Val Ser Glu Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile	
	435 440 445	
15	GGA GCA AGC CTG CTT ACC ATC CTT GAG ATC CTC GAC TAT CTC TGT GAG	1392
	Gly Ala Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp Tyr Leu Cys Glu	
	450 455 460	
20	GTT TTC CAA GAC AGA GTC CTG GGG TAT TTC TGG AAC AGA AGG AGC GCT	1440
	Val Phe Gln Asp Arg Val Leu Gly Tyr Phe Trp Asn Arg Arg Ser Ala	
	465 470 475 480	
25	CAA AAG CGC TCT GGC AAC ACT CTG CTC CAG GAA GAG TTG AAT GGC CAT	1488
	Gln Lys Arg Ser Gly Asn Thr Leu Leu Gln Glu Glu Leu Asn Gly His	
	485 490 495	
30	CGA ACA CAT GTT CCC CAC CTC AGC CTA GGG CCC AGG CCT CCT ACC ACT	1536
	Arg Thr His Val Pro His Leu Ser Leu Gly Pro Arg Pro Pro Thr Thr	
	500 505 510	
35	CCC TGT GCT GTC ACC AAG ACA CTC TCT GCC TCC CAC CGT ACC TGT TAC	1584
	Pro Cys Ala Val Thr Lys Thr Leu Ser Ala Ser His Arg Thr Cys Tyr	
	515 520 525	
40	CTC GTC ACA AGG CTC TAG	1602
	Leu Val Thr Arg Leu *	
	530 533	

INFORMATION CONCERNANT LA SEQ ID NO:6 :

i) CARACTERISTIQUE DE LA SEQUENCE :

A) LONGUEUR 1948 paires de base

B) TYPE : acide nucléique

C) NOMBRE DE BRINS : double

D) CONFIGURATION : linéaire

ii) TYPE DE MOLECULE : ADN

vi) ORIGINE : rat

ix) CARACTERISTIQUE

A) NOM/CLE : MDEG2

B) LOCALISATION : 16 .. 1707

xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:6 :

CCTCGGGCTG AATGA	ATG AGC	CGG AGC	GGC GGA	GCC CGG	CTG CCC	GCG ACC	51
	Met Ser	Arg Ser	Gly Gly	Ala Arg	Leu Pro	Ala Thr	
	1		5		10		
GCG CTC AGC GGC CCG GGA CGC TTC CGT ATG GCC CGC GAG CAG CCG GCG	99						
Ala Leu Ser Gly Pro Gly Arg Phe Arg Met Ala Arg					25	Gln Pro Ala	
	15		20				
CCC GTG GCG GTG GCG GCA GCT AGG CAG CCC GGA GGA GAC CGG AGC GGC	147						
Pro Val Ala Val Ala Ala Ala Arg Gln Pro Gly Gly					40	Asp Arg Ser Gly	
	30		35				
GAT CCG GCG CTG CAG GGG CCA GGG GTC GCC CGC AGG GGG CGG CCG TCC	195						
Asp Pro Ala Leu Gln Gly Pro Gly Val Ala Arg					55	Gly Arg Pro Ser	
	45		50			60	
CTG AGT CGC ACT AAA TTG CAC GGG CTG'CGG CAC ATG TGC GCG GGG CGC	243						
Leu Ser Arg Thr Lys Leu His Gly Leu Arg His Met Cys Ala Gly Arg					70		
		65			75		
ACG GCG GCG GGA GGC TCT TTC CAG CGA CGG GCG CTG TGG GTG CTG GCC	291						
Thr Ala Ala Gly Gly Ser Phe Gln Arg Arg Ala Leu Trp Val Leu Ala					85		
		80				90	
TTC TGC ACG TCC CTC GGC TTG CTG CTG TCC TGG TCC TCG AAC CGC CTG	339						
Phe Cys Thr Ser Leu Gly Leu Leu Ser Trp Ser Ser Asn Arg Leu					100		
		95			105		
CTC TAC TGG CTC AGC TTC CCG TCA CAC ACA CGA GTG CAC CGT GAG TGG	387						
Leu Tyr Trp Leu Ser Phe Pro Ser His Thr Arg					115	Val His Arg Glu Trp	
		110			120		
AGC CGC CAG CTG CCG TTC CCC GCC GTC ACC GTG TGC AAC AAC AAC CCC	435						
Ser Arg Gln Leu Pro Phe Pro Ala Val Thr Val Cys Asn Asn Asn Pro					135		
		125		130		140	
CTG CGC TTC CCG CGC CTC TCC AAG GGG GAC CTC TAC TAC GCG GGC CAC	483						
Leu Arg Phe Pro Arg Leu Ser Lys Gly Asp Leu Tyr Tyr Ala Gly His					150		
		145			155		

	TGG	CTA	GGG	CTG	CTG	CTT	CCC	AAC	CGC	ACC	GCG	CGC	CCG	CTG	GTC	AGC	531
	Trp	Leu	Gly	Leu	Leu	Leu	Pro	Asn	Arg	Thr	Ala	Arg	Pro	Leu	Val	Ser	
				160					165					170			
5	GAG	CTG	CTG	CGG	GGC	GAC	GAG	CCG	CGC	CGC	CAG	TGG	TTC	CGC	AAA	CTG	579
	Glu	Leu	Leu	Arg	Gly	Asp	Glu	Pro	Arg	Arg	Gln	Trp	Phe	Arg	Lys	Leu	
				175				180					185				
10	GCC	GAC	TTC	CGC	CTC	TTC	CTG	CCG	CCG	CGC	CAC	TTC	GAG	GGC	ATC	AGC	627
	Ala	Asp	Phe	Arg	Leu	Phe	Leu	Pro	Pro	Arg	His	Phe	Glu	Gly	Ile	Ser	
				190				195					200				
15	GCT	GCC	TTC	ATG	GAC	CGT	TTG	GGC	CAC	CAG	CTG	GAG	GAT	ATG	CTG	CTC	675
	Ala	Ala	Phe	Met	Asp	Arg	Leu	Gly	His	Gln		Glu	Asp	Met	Leu	Leu	
	205					210					215					220	
	TCC	TGC	AAG	TAC	CGG	GGC	GAG	CTC	TGT	GGC	CCG	CAC	AAC	TTC	TCC	TCA	723
	Ser	Cys	Lys	Tyr	Arg	Gly	Glu	Leu	Cys	Gly	Pro	His	Asn	Phe	Ser	Ser	
					225					230					235		
20	GTG	TTT	ACA	AAA	TAC	GGG	AAG	TGT	TAC	ATG	TTT	AAC	TCA	GGC	GAG	GAT	771
	Val	Phe	Thr	Lys	Tyr	Gly	Lys	Cys	Tyr	Met	Phe	Asn	Ser	Gly	Glu	Asp	
				240					245					250			
25	GGC	AAG	CCG	CTG	CTC	ACC	ACG	GTC	AAG	GGG	GGG	ACG	GGC	AAC	GGG	CTG	819
	Gly	Lys	Pro	Leu	Leu	Thr	Thr	Val	Lys	Gly	Gly	Thr	Gly	Asn	Gly	Leu	
				255				260					265				
30	GAG	ATC	ATG	CTG	GAC	ATT	CAG	CAA	GAT	GAG	TAC	CTG	CCC	ATC	TGG	GGA	867
	Glu	Ile	Met	Leu	Asp	Ile	Gln	Gln	Asp	Glu	Tyr	Leu	Pro	Ile	Trp	Gly	
				270			275					280					
35	GAG	ACA	GAG	GAA	ACA	ACG	TTT	GAA	GCA	GGA	GTG	AAG	GTT	CAG	ATC	CAC	915
	Glu	Thr	Glu	Glu	Thr	Phe	Glu	Ala	Gly	Val	Lys	Val	Gln	Ile	His		
				285			290				295				300		
40	AGT	CAG	TCT	GAG	CCG	CCT	TTC	ATC	CAA	GAG	CTG	GGC	TTT	GGG	GTG	GCT	963
	Ser	Gln	Ser	Glu	Pro	Pro	Phe	Ile	Gln	Glu	Leu	Gly	Phe	Gly	Val	Ala	
					305					310					315		
45	CCG	GGG	TTC	CAG	ACC	TTC	GTG	GCC	ACA	CAA	GAG	CAG	AGG	CTC	ACA	TAT	1011
	Pro	Gly	Phe	Gln	Thr	Phe	Val	Ala	Thr	Gln	Glu	Gln	Arg	Leu	Thr	Tyr	
				320				325						330			
50	CTG	CCC	CCA	CCA	TGG	GGG	GAG	TGC	CGG	TCC	TCA	GAG	ATG	GGA	CTC	GAC	1059
	Leu	Pro	Pro	Pro	Trp	Gly	Glu	Cys	Arg	Ser	Ser	Glu	Met	Gly	Leu	Asp	
				335				340					345				
55	TTC	TTT	CCT	GTT	TAC	AGC	ATC	ACA	GCC	TGT	CGG	ATT	GAC	TGT	GAG	ACC	1107
	Phe	Phe	Pro	Val	Tyr	Ser	Ile	Thr	Ala	Cys	Arg	Ile	Asp	Cys	Glu	Thr	
				350			355					360					
55	CGC	TAC	ATC	GTG	GAG	AAC	TGT	AAC	TGC	CGC	ATG	GTC	CAC	ATG	CCA	GGG	1155
	Arg	Tyr	Ile	Val	Glu	Asn	Cys	Asn	Cys	Arg	Met	Val	His	Met	Pro	Gly	
						370					375					380	

	GAC GCC CCT TTC TGC ACC CCT GAG CAG CAC AAG GAG TGT GCA GAG CCT	1203
	Asp Ala Pro Phe Cys Thr Pro Glu Gln His Lys Glu Cys Ala Glu Pro	
	385 390 395	
5	GCC CTC GGT CTA CTG GCA GAA AAG GAC AGC AAT TAC TGT CTC TGC AGG	1251
	Ala Leu Gly Leu Leu Ala Glu Lys Asp Ser Asn Tyr Cys Leu Cys Arg	
	400 405 410	
10	ACA CCC TGC AAC CTG ACA CGC TAC AAC AAA GAG CTC TCC ATG GTG AAG	1299
	Thr Pro Cys Asn Leu Thr Arg Tyr Asn Lys Glu Leu Ser Met Val Lys	
	415 420 425	
15	ATC CCC AGC AAG ACG TCA GCC AAG TAC TTA GAG AAG AAA TTT AAC AAA	1347
	Ile Pro Ser Lys Thr Ser Ala Lys Tyr Leu Glu Lys Phe Asn Lys	
	430 435 440	
	TCG GAA AAA TAT ATC TCA GAG AAC ATT CTT GTT CTG GAC ATA TTT TTT	1395
	Ser Glu Lys Tyr Ile Ser Glu Asn Ile Leu Val Leu Asp Ile Phe Phe	
	445 450 455 460	
20	GAG GCG CTC AAT TAC GAA ACA ATT GAA CAG AAG AAG GCG TAT GAA GTT	1443
	Glu Ala Leu Asn Tyr Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Val	
	465 470 475	
25	GCT GCC TTA CTT GGT GAC ATC GGT GGT CAG ATG GGA CTG TTC ATT GGT	1491
	Ala Ala Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly	
	480 485 490	
30	GCT AGT CTC CTC ACA ATA CTA GAG CTC TTT GAT TAT ATT TAT GAG CTG	1539
	Ala Ser Leu Leu Thr Ile Leu Glu Leu Phe Asp Tyr Ile Tyr Glu Leu	
	495 500 505	
35	ATC AAA GAG AAG CTA TTA GAC CTG CTT GGC AAA GAA GAA GAG GAA GGG	1587
	Ile Lys Glu Lys Leu Leu Asp Leu Leu Gly Lys Glu Glu Glu Glu Gly	
	510 515 520	
40	AGC CAC GAT GAG AAC ATG AGC ACC TGT GAC ACA ATG CCA AAC CAC TCT	1635
	Ser His Asp Glu Asn Met Ser Thr Cys Asp Thr Met Pro Asn His Ser	
	525 530 535 540	
	GAA ACC ATC AGC CAC ACT GTG AAC GTG CCC CTG CAG ACA GCT TTG GGC	1683
	Glu Thr Ile Ser His Thr Val Asn Val Pro Leu Gln Thr Ala Leu Gly	
	545 550 555	
45	ACC CTG GAG GAG ATT GCC TGC TGA CACCTCTCAG GCAACGCAGC ACCTCCAAAC	1737
	Thr Leu Glu Glu Ile Ala Cys *	
	560 563	
50	AGACCTTAAA GGCCCAAGAC CTAGGACAGG AGACAGCAAG CGCAGGTGGG ATCGCCCTCG	1797
	ACGACTGAAA GAAGCAGAGC CCCCATATG CACACATTGC GAACTTCTGC CAAACCTCAC	1857
	CTGGCCACAT CTGACATGAA CCGTCCCGGG CCTTCGCTCA TGTCCCTCGC AGGACCGATG	1917
	AGTCGCACTC CGGAACCTGTC CAAGAACATA C	1948